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PATENT APPLICATION: US/10/081,969   TIME: 09:38:48

Input Set : **A:\31704A.ST25.txt**
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 3 <110> APPLICANT: Cheng, Cheng
 4         Clarke, Lori
 5         Connelly, Sheila
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 7         Forry-Schaudies, Suzanne
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 9         Hallenbeck, Paul
10         Hay, Carl
11         Jakubczak, John
12         Kaleko, Michael
13         Phipps, Sandrina
14         Police, Seshidhar
15         Ryan, Patricia
16         Steward, David
17         Xie, Yuefeng
19 <120> TITLE OF INVENTION: Novel Oncolytic Adenoviral Vectors
21 <130> FILE REFERENCE: 4-31704A/GTI
23 <140> CURRENT APPLICATION NUMBER: US 10/081,969
24 <141> CURRENT FILING DATE: 2002-02-22
26 <150> PRIOR APPLICATION NUMBER: US 60/270,922
27 <151> PRIOR FILING DATE: 2001-02-23
29 <150> PRIOR APPLICATION NUMBER: US 60/295,037
30 <151> PRIOR FILING DATE: 2001-06-01
32 <150> PRIOR APPLICATION NUMBER: US 60/348,670
33 <151> PRIOR FILING DATE: 2000-01-14
35 <160> NUMBER OF SEQ ID NOS: 98
37 <170> SOFTWARE: PatentIn version 3.1
39 <210> SEQ ID NO: 1
40 <211> LENGTH: 140
41 <212> TYPE: DNA
42 <213> ORGANISM: Simian virus 40
44 <220> FEATURE:
45 <221> NAME/KEY: misc_feature
46 <222> LOCATION: (1)..(140)
47 <223> OTHER INFORMATION:
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51 <222> LOCATION: (1)..(140)
52 <223> OTHER INFORMATION: Fig. 1 A
55 <400> SEQUENCE: 1
56 cttatcgata ccgtcgaaac ttgtttattg cagcttataa tggttacaaa taaagcaaca       60
58 caaatttcac aaataaagca ttttttttcac tgcattctag ttgtggtttg tccaaactca      120
60 tcaatgtatc ttatcatgtc                                                    140
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64 <211> LENGTH: 600
65 <212> TYPE: DNA
66 <213> ORGANISM: Human adenovirus type 5
68 <220> FEATURE:
69 <221> NAME/KEY: misc_feature
70 <222> LOCATION: (1)..(600)
71 <223> OTHER INFORMATION: Fig. 2- E1A transcrition control region
74 <400> SEQUENCE: 2
75 catcatcaat aatatacctt attttggatt gaagccaata tgataatgag ggggtggagt      60
77 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagtagtgtg gcggaagtgt     120
79 gatgttgcaa gtgtggcgga acacatgtaa gcgacggatg tggcaaaagt gacgtttttg     180
81 gtgtgcgccg gtgtacacag gaagtgacaa ttttcgcgcg gttttaggcg gatgttgtag     240
83 taaatttggg cgtaaccgag taagatttgg ccattttcgc gggaaaactg aataagagga     300
85 agtgaaatct gaataatttt gtgttactca tagcgcgtaa tatttgtcta gggccgcggg     360
87 gactttgacc gtttacgtgg agactcgccc aggtgttttt ctcaggtgtt ttccgcgttc     420
89 cgggtcaaag ttggcgtttt attattatag tcagctgacg tgtagtgtat ttatacccgg     480
91 tgagttcctc aagaggccac tcttgagtgc cagcgagtag agttttctcc tccgagccgc     540
93 tccgacaccg ggactgaaaa tgagacatat tatctgccac ggaggtgtta ttaccgaaga     600
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 1802
98 <212> TYPE: DNA
99 <213> ORGANISM: artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: viral vector construct
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (1)..(1802)
107 <223> OTHER INFORMATION:
109 <220> FEATURE: ·
110 <221> NAME/KEY: misc_feature
111 <222> LOCATION: (1)..(1802)
112 <223> OTHER INFORMATION: Fig. 3 A-Left end of Ar6pAE2fF sequence
115 <400> SEQUENCE: 3
116 catcatcaat aatatacctt attttggatt gaagccaata tgataatgag ggggtggagt      60
118 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagggcgcga tcaagcttat     120
120 cgataccgtc gaaacttgtt tattgcagct tataatggtt acaaataaag caatagcatc     180
122 acaaatttca caaataaagc attttttttca ctgcattcta gttgtggttt gtccaaactc     240
124 atcaatgtat cttatcatgt ctggatccgc gccgctagcg atcatccgga caaagcctgc     300
126 gcgcgccccg ccccgccatt ggccgtaccg ccccgcgccg ccgccccatc tcgcccctcg     360
128 ccgccgggtc cggcgcgtta aagccaatag gaaccgccgc cgttgttccc gtcacggccg     420
130 gggcagccaa ttgtggcggc gctcggcggc tcgtggctct ttcgcggcaa aaaggatttg     480
132 gcgcgtaaaa gtggccggga ctttgcaggc agcggcggcc ggggcggag cgggatcgag     540
134 ccctcgatga tatcagatca tcggatcccg gtcgactgaa aatgagacat attatctgcc     600
136 acggaggtgt tattaccgaa gaaatggccg ccagtctttt ggaccagctg atcgaagagg     660
138 tactggctga taatcttcca cctcctagcc attttgaacc acctacccott cacgaactgt     720
140 atgatttaga cgtgacggcc cccgaagatc ccaacgagga ggcggtttcg cagatttttc     780
142 ccgactctgt aatgttggcg gtgcaggaag ggattgactt actcacttt ccgccggcgc     840
144 ccggttctcc ggagccgcct cacctttccc ggcagcccga gcagccggag cagagagcct     900
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146 tgggtccggt ttctatgcca aaccttgtac cggaggtgat cgatcttacc tgccacgagg   960
148 ctggctttcc acccagtgac gacgaggatg aagagggtga ggagtttgtg ttagattatg   1020
150 tggagcaccc cgggcacggt tgcaggtctt gtcattatca ccggaggaat acgggggacc   1080
152 cagatattat gtgttcgctt tgctatatga ggacctgtgg catgtttgtc tacagtaagt   1140
154 gaaaattatg ggcagtgggt gatagagtgg tgggtttggt gtggtaattt ttttttttaat 1200
156 ttttacagtt ttgtggttta aagaattttg tattgtgatt tttttaaaag gtcctgtgtc   1260
158 tgaacctgag cctgagcccg agccagaacc ggagcctgca agacctaccc gccgtcctaa   1320
160 aatggcgcct gctatcctga gacgcccgac atcacctgtg tctagagaat gcaatagtag   1380
162 tacggatagc tgtgactccg gtccttctaa cacacctcct gagatacacc cggtggtccc   1440
164 gctgtgcccc attaaaccag ttgccgtgag agttggtggg cgtcgccagg ctgtggaatg   1500
166 tatcgaggac ttgcttaacg agcctgggca acctttggac ttgagctgta aacgccccag   1560
168 gccataaggt gtaaacctgt gattgcgtgt gtggttaacg cctttgtttg ctgaatgagt   1620
170 tgatgtaagt ttaataaagg gtgagataat gtttaacttg catggcgtgt aaatgggggc   1680
172 ggggcttaaa gggtatataa tgcgccgtgg gctaatcttg gttacatctg acctcatgga   1740
174 ggcttgggag tgtttggaag attttttctgc tgtgcgtaac ttgctggaac agagctctaa 1800
176 ca   1802
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 532
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Viral vector sequence
187 <220> FEATURE:
188 <221> NAME/KEY: misc_feature
189 <222> LOCATION: (1)..(532)
190 <223> OTHER INFORMATION: Fig. 3 B- right end of of Arp6AE2fF sequence
193 <400> SEQUENCE: 4
194 aacctacgcc cagaaacgaa agccaaaaaa cccacaactt cctcaaatcg tcacttccgt   60
196 tttcccacgt tacgtcactt cccattttaa ttaagaattc tacaattccc aacacataca   120
198 agttactccg ccctaaaacc ctgggcgagt ctccacgtaa acggtcaaag tccccgcggc   180
200 cctagacaaa tattacgcgc tatgagtaac acaaaattat tcagatttca cttcctctta   240
202 ttcagttttc ccgcgaaaat ggccaaatct tactcggtta cgcccaaatt tactacaaca   300
204 tccgcctaaa accgcgcgaa aattgtcact tcctgtgtac accggcgcac accaaaaacg   360
206 tcacttttgc cacatccgtc gcttacatgt gttccgccac acttgcaaca tcacacttcc   420
208 gccacactac tacgtcacc gcccc gttcc cacgccccgc gccacgtcac aaactccacc   480
210 ccctcattat catattggct tcaatccaaa ataaggtata ttattgatga tg   532
213 <210> SEQ ID NO: 5
214 <211> LENGTH: 660
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Viral vector construct
221 <220> FEATURE:
222 <221> NAME/KEY: misc_feature
223 <222> LOCATION: (1)..(660)
224 <223> OTHER INFORMATION: Fig. 4-Left end of Ar6F sequence
227 <400> SEQUENCE: 5
228 catcatcaat aatatacctt attttggatt gaagccaata tgataatgag ggggtggagt   60
230 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagggcgcgc cgctagcgat   120

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232 atcggatccc ggtcgactga aaatgagaca tattatctgc cacggaggtg ttattaccga   180
234 agaaatggcc gccagtcttt tggaccagct gatcgaagag gtactggctg ataatcttcc   240
236 acctcctagc cattttgaac cacctaccct tcacgaactg tatgatttag acgtgacggc   300
238 ccccgaagat cccaacgagg aggcggtttc gcagattttt cccgactctg taatgttggc   360
240 ggtgcaggaa gggattgact tactcacttt tccgccggcg cccggttctc cggagccgcc   420
242 tcacctttcc cggcagcccg agcagccgga gcagagagcc ttgggtccgg tttctatgcc   480
244 aaaccttgta ccggaggtga tcgatcttac ctgccacgag gctggctttc cacccagtga   540
246 cgacgaggat gaagagggtg aggagtttgt gttagattat gtggagcacc ccgggcacgg   600
248 ttgcaggtct tgtcattatc accggaggaa tacggggggac ccagatatta tgtgttcgct   660
251 <210> SEQ ID NO: 6
252 <211> LENGTH: 660
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Fig. 5- left end of Ar6pAF sequence
259 <220> FEATURE:
260 <221> NAME/KEY: misc_feature
261 <222> LOCATION: (1)..(660)
262 <223> OTHER INFORMATION: Fig. 5- left end of Ar6pAF sequence
265 <400> SEQUENCE: 6
266 catcatcaat aatatacctt attttggatt gaagccaata tgataatgag ggggtggagt    60
268 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagggcgcga tcaagcttat   120
270 cgataccgtc gaaacttgtt tattgcagct tataatggtt acaaataaag caatagcatc   180
272 acaaatttca caaataaagc attttttttca ctgcattcta gttgtggttt gtccaaactc   240
274 atcaatgtat cttatcatgt ctggatccgc gccgctagcg atatcggatc ccggtcgact   300
276 gaaaatgaga catattatct gccacggagg tgttattacc gaagaaatgg ccgccagtct   360
278 tttggaccag ctgatcgaag aggtactggc tgataatctt ccacctccta gccattttga   420
280 accacctacc cttcacgaac tgtatgattt agacgtgacg gccccccgaag atcccaacga   480
282 ggaggcggtt tcgcagattt ttcccgactc tgtaatgttg gcggtgcagg aagggattga   540
284 cttactcact tttccgccgg cgcccggttc tccggagccg cctcaccttt cccggcagcc   600
286 cgagcagccg gagcagagag ccttgggtcc ggtttctatg ccaaaccttg taccggaggt   660
289 <210> SEQ ID NO: 7
290 <211> LENGTH: 949
291 <212> TYPE: DNA
292 <213> ORGANISM: Murine
294 <220> FEATURE:
295 <221> NAME/KEY: CDS
296 <222> LOCATION: (182)..(640)
297 <223> OTHER INFORMATION:
299 <400> SEQUENCE: 7
300 ttccggacag acctcaataa ctctgtttac cagaacagga ggtgagctta gaaaacccttt    60
302 agggtattag gccaaaggcg cagctactgt ggggtttatg aacaattcaa gcaactctac   120
304 gggctattct aattcaggtt tctctagccg ggctgcagga attcgatggc cgctacctac   180
306 a atg gcc cac gag aga aag gct aag gtc ctg agg agg atg tgg ctg cag   229
307   Met Ala His Glu Arg Lys Ala Lys Val Leu Arg Arg Met Trp Leu Gln
308   1               5                   10                  15
310 aat tta ctt ttc ctg ggc att gtg gtc tac agc ctc tca gca ccc acc   277
311 Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser Leu Ser Ala Pro Thr
312              20                  25                  30
```

```
314 cgc tca ccc atc act gtc acc cgg cct tgg aag cat gta gag gcc atc    325
315 Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His Val Glu Ala Ile
316         35                  40                  45
318 aaa gaa gcc ctg aac ctc ctg gat gac atg cct gtc aca ttg aat gaa    373
319 Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val Thr Leu Asn Glu
320         50                  55                  60
322 gag gta gaa gtc gtc tct aac gag ttc tcc ttc aag aag cta aca tgt    421
323 Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys Lys Leu Thr Cys
324 65                  70                  75                  80
326 gtg cag acc cgc ctg aag ata ttc gag cag ggt cta cgg ggc aat ttc    469
327 Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu Arg Gly Asn Phe
328                 85                  90                  95
330 acc aaa ctc aag ggc gcc ttg aac atg aca gcc agc tac tac cag aca    517
331 Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser Tyr Tyr Gln Thr
332                 100                 105                 110
334 tac tgc ccc cca act ccg gaa acg gac tgt gaa aca caa gtt acc acc    565
335 Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr Gln Val Thr Thr
336                 115                 120                 125
338 tat gcg gat ttc ata gac agc ctt aaa acc ttt ctg act gat atc ccc    613
339 Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu Thr Asp Ile Pro
340         130                 135                 140
342 ttt gaa tgc aaa aaa cca gtc caa aaa tgaggaagcc caggccagct          660
343 Phe Glu Cys Lys Lys Pro Val Gln Lys
344 145                 150
346 ctgaatccag cttctcagac tgctgctttt gtgcctgcgt aatgagccag gaactcggaa    720
348 tttctgcctt aaagggacca agagatgtgg cacaggtagt cgaatcaagc ttatcgatac    780
350 cgtcgacctc gactagataa cttcgtataa tgtatgctat acgaagttat gctagaaatg    840
352 gacggaatta ttacagagca gcgcctgcta gaaagacgca gggcagcggc cgagcaacag    900
354 cgcatgaatc aagagctcca agacatggtt aacttgcacc agtgcaaaa             949
357 <210> SEQ ID NO: 8
358 <211> LENGTH: 153
359 <212> TYPE: PRT
360 <213> ORGANISM: Murine
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364 Met Ala His Glu Arg Lys Ala Lys Val Leu Arg Arg Met Trp Leu Gln
365 1               5                   10                  15
368 Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser Leu Ser Ala Pro Thr
369                 20                  25                  30
372 Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His Val Glu Ala Ile
373         35                  40                  45
376 Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val Thr Leu Asn Glu
377         50                  55                  60
380 Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys Lys Leu Thr Cys
381 65                  70                  75                  80
384 Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu Arg Gly Asn Phe
385                 85                  90                  95
388 Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser Tyr Tyr Gln Thr
389                 100                 105                 110
392 Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr Gln Val Thr Thr
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